are supported by the disclosure as originally filed. Accordingly, entry of these amendments is respectfully requested.

Additionally, claim 5 is amended to correct a typographical error by correcting the amino acid at position +96 from "lysine' to "leucine". The amendment to correct the typographical error in claim 5 does not introduce new matter and is supported by the specification (Figure 3) as originally filed. Accordingly, entry of the amendment to claim 5 is respectfully requested.

The changes in the specification do not involve new matter and entry of them is respectfully requested. If a telephone interview would be of assistance in advancing the prosecution of the subject application, applicants' undersigned attorney invites the Examiner to telephone her at the number provided below.

No additional fee is deemed necessary in connection with the filing of this Amendment. If any additional fees are necessary, the Patent Office is authorized to charge any additional fee to Deposit Account No. 50-0306.

Respectfully submitted,

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MARKED-UP VERSION TO SHOW AMENDMENT OF SPECIFICATION

Please amend the claims to read as follows:

--2. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 [has] comprises one or more mutations in a region S25-R33 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 51-59), and wherein the mutation is a substitution of any amino acid beginning with [of] serine at position +25 of Figure 3 (SEQ ID NO.: 2, at position 51) and ending with [through] lysine at position +28 of Figure 3 (SEQ ID NO.: 2, at position 54) with a different amino acid selected from alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

--3. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 [has] comprises a [one or more] mutation[s] in a region S25-R33 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 51-59), and wherein the mutation is a substitution of alanine at position +29 of Figure 3 (SEQ ID NO.: 2, at position 55) with any of arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, or valine. --

--4. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 [has] comprises one or more mutations in a region S25-R33 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 51-59), and wherein the mutation is a substitution of any amino acid beginning with [of] threonine at position +30 of Figure 3 (SEQ ID NO.: 2, at position 56) and ending with [through] arginine at position +33 of Figure 3 (SEQ ID NO.: 2, at position 59) with a different amino acid selected from alanine, arginine, asparagine,

aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine.--

--5. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 [has] comprises one or more mutations in a region E95-G107 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 121-133), and wherein the mutation is a substitution of any amino acid beginning with [of] glutamic acid at position +95 of Figure 3 (SEQ ID NO.: 2, at position 121) and ending with [through] leucine at position +96 of Figure 3 (SEQ ID NO.: 2, at position 122) with a different amino acid selected from alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

--6. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 [has] comprises one or more mutations in a region E95-G107 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 121-133), and wherein the mutation is a substitution of any amino acid beginning with [of] methionine at position +97 of Figure 3 (SEQ ID NO.: 2, at position 123) and ending with [through] tyrosine at position +103 of Figure 3 (SEQ ID NO.: 2, at position 129) with a different amino acid selected from alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

--7. (Amended) The soluble CTLA4 mutant molecule of claim [5] 6, wherein the mutation is a substitution of tyrosine at position +103 of Figure 3 (SEQ ID NO.: 2, at position 129) with a different amino acid selected from a group consisting of arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine,

histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, [tyrosine,] and valine. --

--8. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 [has] comprises one or more mutations in a region E95-G107 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 121-133), and wherein the mutation is a substitution of any amino acid beginning with [of] leucine at position +104 of Figure 3 (SEQ ID NO.: 2, at position 130) and ending with [through] glycine at position +107 of Figure 3 (SEQ ID NO.: 2, at position 133) with a different amino acid selected from alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

--9. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 [has] comprises one or more mutations in a region N108-I115 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 134-141), and wherein the mutation is a substitution of any amino acid beginning with asparagine at position +108 of Figure 3 (SEQ ID NO.: 2, at position 134) and ending with [at] isoleucine at position +115 [(N108-I115)] of Figure 3 (SEQ ID NO.: 2, at position 141) with a different amino acid selected from a group consisting of alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

--20. (Amended) The method of claim 19, wherein the soluble CTLA4 mutant molecule is any of L104EA29L (SEQ ID NO.: 16), L104EA29T (SEQ ID NO.: 18), or L104EA29W (SEQ ID NO.: 20).